

FIG. 1

CGGGGGGGGATACCCAGAGATGGGGTTCGAGGAGAGACCCGGGAGTAGAGAGAGAACTCACTC	71
CCCGAGTCCCGACCCCTCCCAAGCAAGGTTATAATATACTTATCTCTCATGCTTTTCTGCCCCCTT	142
CTCCCCAAATCATCAACAATAGAGAAGAAACATG TCA GGA CAC AAA TGC AGT TAT CCC	205
Met Ser Gly His Lys Cys Ser Tyr Pro	9
TGG GAC TTA CAG GAT CGA TAT GCT CAA GAT AAG TCA G'IT' G'IA AAT' AAG ATG CAA	259
Trp Asp Leu Gln Asp Arg Tyr Ala Gln Asp Lys Ser Val Val Asn Lys Met Gln	27
CAG AGA TAT TGG GAG ACG AAG CAG GCC TTT ATT AAA GCC ACA GGG AAG AAG GAA	313
Gln Arg Tyr Trp Glu Thr Lys Lys Gln Ala Phe Ile Lys Ala Thr Gly Lys Lys Glu	45
GAT GAA CAT GTT GTT GCC TCT GAC GCG GAC CTG GAT GCC AAG CTA GAG CTG TTT	367
Asp Glu His Val Val Ala Ser Asp Ala Asp Leu Asp Ala Lys Leu Glu Leu Phe	63
CAT TCA ATT CAG AGA ACC TGT CTG GAC TTA TCG AAA GCA ATT GTA CTC TAT CAA	421
His Ser Ile Gln Arg Thr Cys Leu Asp Leu Ser Lys Ala Ile Val Leu Tyr Gln	81
AAG AGG ATA TGT TTC TTT TTT TTT CAA GAA AAC GAA CTG GGA AAA TTT CTT CGA	475
Lys Arg Ile Cys Phe Leu Ser Gln Glu Glu Asn Glu Leu Gly Lys Phe Leu Arg	99
TCC CAA GGT TTC CAA GAT AAA ACC AGA GCA GGA AAG ATG ATG CAA GCG ACA GGA	529
Ser Gln Gly Phe Gln Asp Lys Thr Arg Ala Gly Lys Met Met Gln Ala Thr Gly	117
AAG GCC CTC TGC TTT TCT TCC CAG CAA AGG TTG GCC TTA CGA AAT CCT TTG TGT	583
Lys Ala Leu Cys Phe Ser Ser Gln Gln Arg Leu Ala Leu Arg Asn Pro Leu Cys	135
CGA TTT CAC CAA GAA GTG GAG ACT TTT CGG CAT CGG GCC ATC TCA GAT ACT TGG	637
Arg Phe His Gln Glu Val Glu Thr Phe Arg His Arg Ala Ile Ser Asp Thr Trp	153
CTG ACG GTG AAC CGC ATG GAA CAG TGC AGG ACG GAA TAT AGA GGA GCA CTA TTA	691
Leu Thr Val Asn Arg Met Glu Gln Cys Arg Thr Glu Tyr Arg Gly Ala Leu leu	171

FIG. 2A

TGG	ATG	AAG	GAC	GTG	TCT	CAG	GAG	CTT	GAT	CCA	GAC	CTC	TAC	AAG	CAA	ATG	GAG	745
Trp	Met	Lys	Asp	Val	Ser	Gln	Glu	Leu	Asp	Pro	Asp	Leu	Tyr	Lys	Gln	Met	Glu	189
AAG	TTC	AGG	AAG	GTG	CAA	ACA	CAA	GTG	CGC	CTT	GCA	AAA	AAA	AAA	AAA	AAA	AAA	799
Lys	Phe	Arg	Lys	Val	Gln	Thr	Gln	Val	Arg	Leu	Ala	Lys	Lys	Asn	Phe	Asp	Lys	207
TTG	AAG	ATG	GAT	GTG	TGT	CAA	AAA	GTG	GAT	CTT	CTT	GGA	GCG	AGC	AGA	TGC	AAT	853
Leu	Lys	Met	Asp	Val	Cys	Gln	Lys	Val	Asp	Leu	Leu	Gly	Ala	Ser	Arg	Cys	Asn	225
CTC	TTG	TCT	CAC	ATG	CTA	GCA	ACA	TAC	CAG	ACC	ACT	CTG	CTT	CAT	TTT	TGG	GAG	907
Leu	Leu	Ser	His	Met	Leu	Ala	Thr	Tyr	Gln	Thr	Thr	Leu	Leu	His	Phe	Trp	Glu	243
AAA	ACT	TCT	CAC	ACT	ATG	GCA	GCC	ATC	CAT	GAG	AGT	TTC	AAA	GGT	TAT	CAA	CCA	961
Lys	Thr	Ser	His	Thr	Met	Ala	Ala	Ile	His	Glu	Ser	Phe	Lys	Gly	Tyr	Gln	Pro	261
TAT	GAA	TTT	ACT	ACT	TTA	AAG	AGC	TTA	CAA	GAC	CCT	ATG	AAA	AAA	TTA	GTT	GAG	1015
Tyr	Glu	Phe	Thr	Thr	Leu	Lys	Ser	Leu	Gln	Asp	Pro	Met	Lys	Lys	Leu	Val	Glu	279
AAA	GAA	GAG	AAG	AAG	AAA	ATC	AAC	CAG	CAG	GAA	AGT	ACA	GAT	GCA	GCC	GTG	CAG	1069
Lys	Glu	Glu	Lys	Lys	Lys	Ile	Asn	Gln	Gln	Glu	Ser	Thr	Asp	Ala	Ala	Val	Gln	297
GAG	CCG	AGC	CAA	TTA	ATT	TCA	TTA	GAG	GAA	GAA	AAC	CAG	CGC	AAG	GAA	TCC	TCT	1123
Glu	Pro	Ser	Ser	Gln	Leu	Ile	Ser	Leu	Glu	Glu	Glu	Asn	Arg	Lys	Glu	Ser	Ser	315
PKC																		
AGT	TTT	AAG	ACT	GAA	GAT	GGA	AAA	AGT	ATT	TTA	TCT	GCC	TTA	GAC	AAA	GGC	TCT	1177
Ser	Phe	Lys	Thr	Glu	Asp	Gly	Lys	Ser	Ile	Leu	Ser	Ala	Leu	Asp	Lys	Gly	Ser	333
ACA	CAT	ACT	GCA	TGC	TCA	GGA	CCC	ATA	GAT	GAA	CTA	TTA	GAC	ATG	AAA	TCT	GAG	1231
Thr	His	Thr	Ala	Cys	Ser	Gly	Pro	Ile	Asp	Glu	Leu	Leu	Asp	Met	Lys	Ser	Glu	351

FIG. 2B

GAA GGT GCT TGC CTG GGA Glu Gly Ala Cys Leu Gly	CCA GTG GCA GGG ACC CCG GAA CCT GAA GGT GCT GAC	1285 369
AAA GAT GAC CTG CTG CTG Lys Asp Asp Leu Leu Leu	Pro Val Ala Gly Thr Pro Glu Pro Glu Glu Glu Glu * CK2	1339 387
GGC GAG TTC AGC AAA GAG Gly Glu Phe Ser Lys Glu	TTG AGT GAG ATC TTC AAT GCT TCC TCC TTG GAA GAG TTC Phe Asn Ala Ser Ser Leu Glu Glu	1393 405
CCA GTG CCC ACT ATG GCC Pro Val Pro Thr Met Ala	TGG GCC GCT GTG TTT GGA GAC GGC CAA GTG AAG GAG Trp Ala Val Phe Gly Asp Gly Gln Val Lys Glu	1447 423
GGT TTC CTT CCT TCG CAG Gly Phe Leu Pro Ser Gln	CTT TTA GAC CAA AAT ATG AAA GAC TTA CAG GCC TCG Leu Leu Leu Asp Gln Asn Met Lys Asp Leu Gln Ala Ser CK2	1501 441
CTA CAA GAA CCT GCT AAG Leu Gln Glu Pro Ala Lys	GCT GCC TCA GAC CTG ACT GCC TGG TTC AGC CTC TTC Ala Ala Ser Asp Leu Thr Ala Trp Phe Ser Leu Phe CK2	1555 459
GCT GAC CTC GAC CCA CTC Ala Asp Leu Asp Pro Leu	TCA AAT CCT GAT GCT GTT GGG AAA ACC GAT AAA GAA Ser Asn Pro Asp Ala Val Gly Lys Thr Asp Lys Glu	1609 477
CAC GAA TTG CTC AAT GCA His Glu Leu Leu Asn Ala	TGAATCTGTACCCTTCGGAGGGCACTCACATGCCGCCCCAGCAGCT END	1674 483
CCCCCTGGGGCTAGCAGAAGTATAAAGTGATCAGTATGCTGTTTAAATAATTATGTGCCATTTTAAATAAAA TGAAAGGGTCAACGGCCCTGTATAAAAAA		1745 1785

FIG. 2C

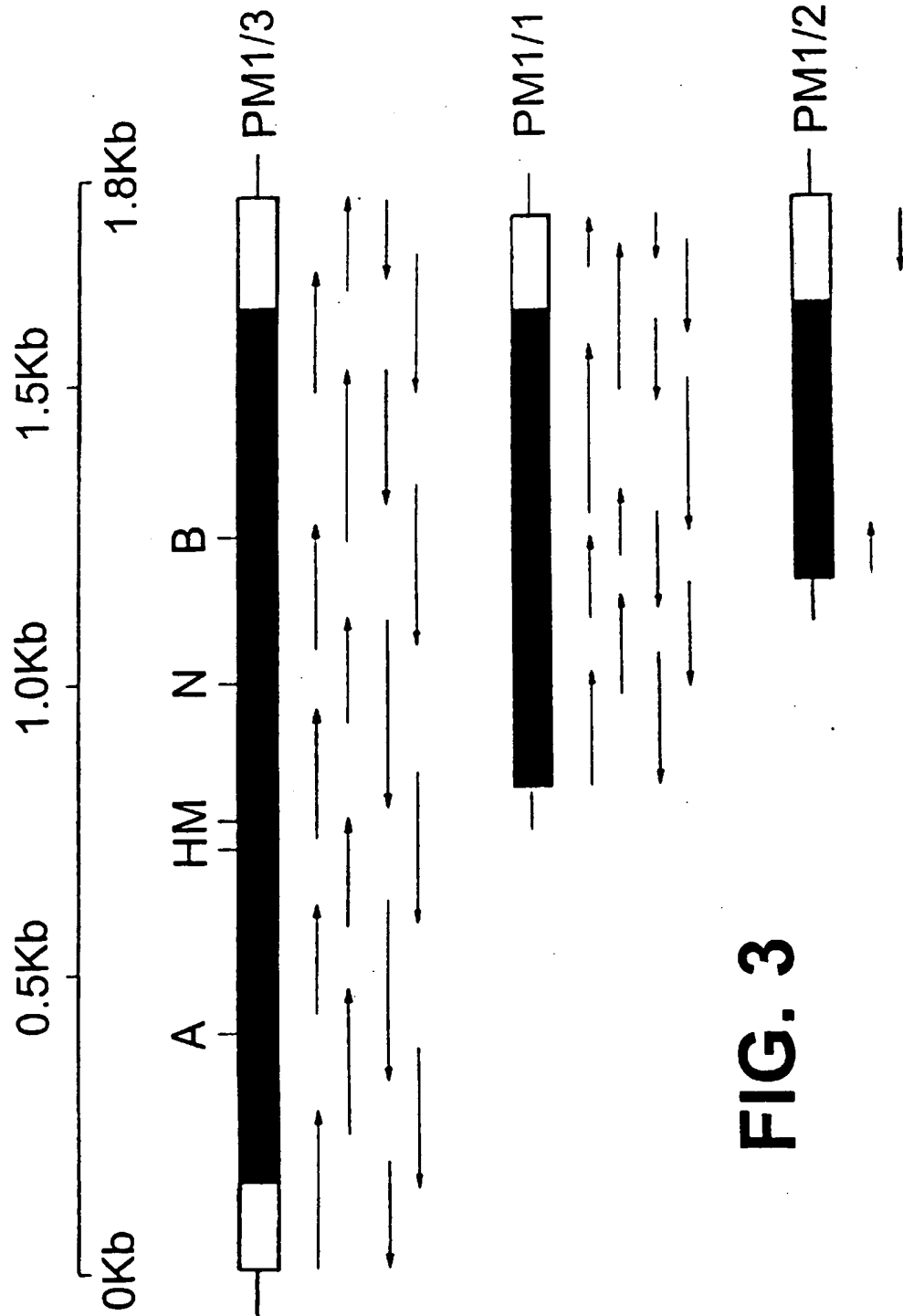


FIG. 3

N	F	D	K	L	K	M	D	V	C	PM-1	205
V	F	D	K	L	K	H	L	V	D	BSA	373

S	E	E	G	A	C	L	G	P	V	PM-1	351
E	D	K	G	A	C	L	L	P	K	BSA	172

FIG. 4

PM-1 Kyte and Doolittle Hydropathy Analysis

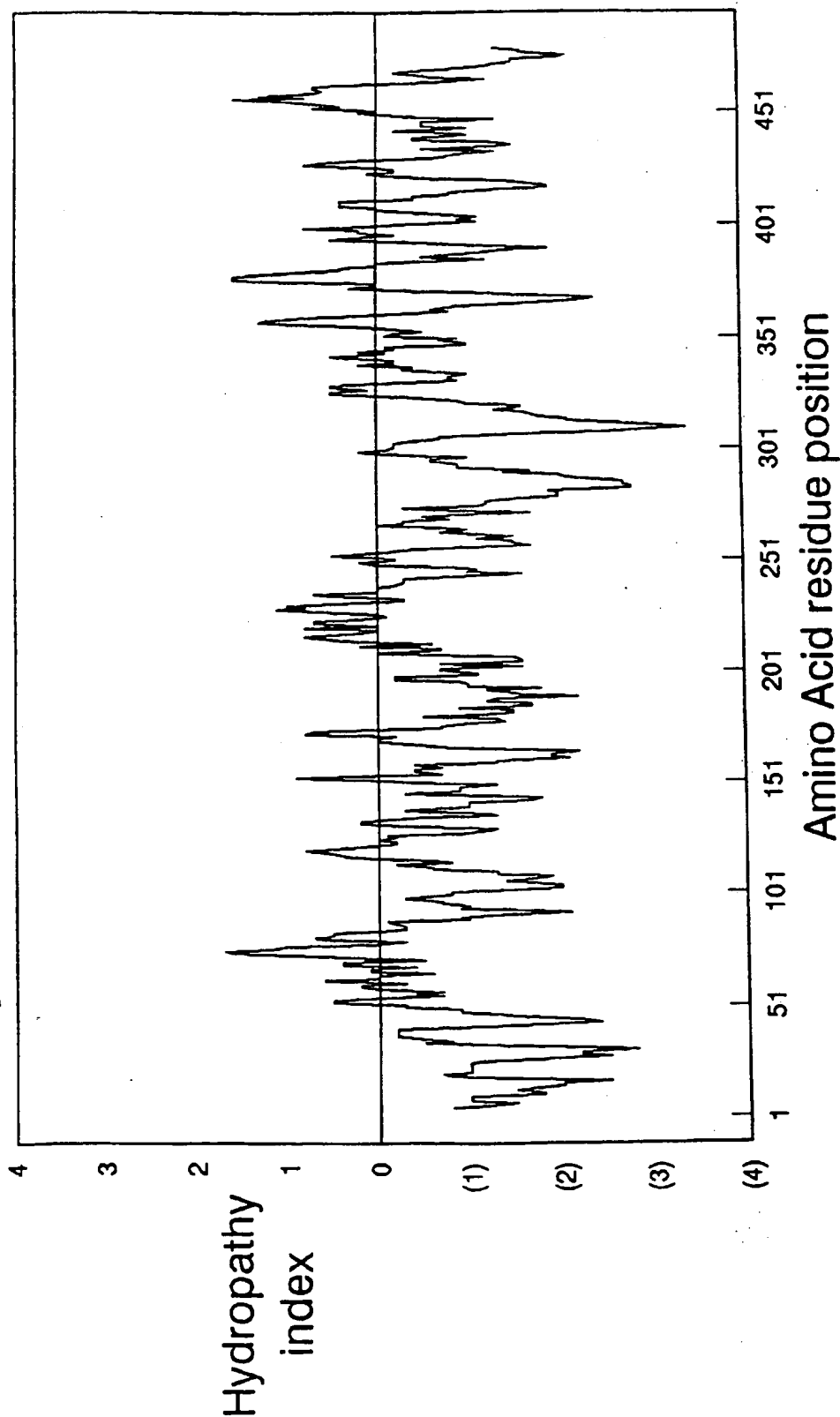


FIG. 5

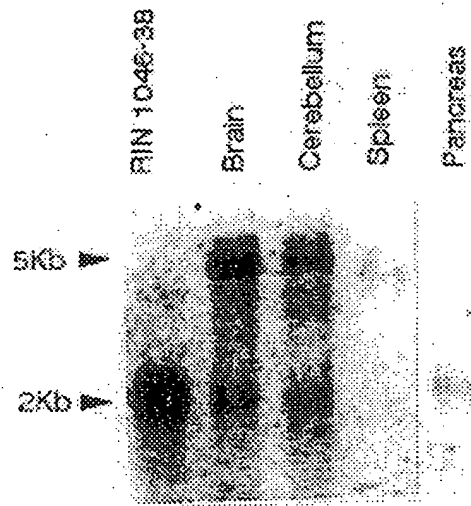


FIG. 6

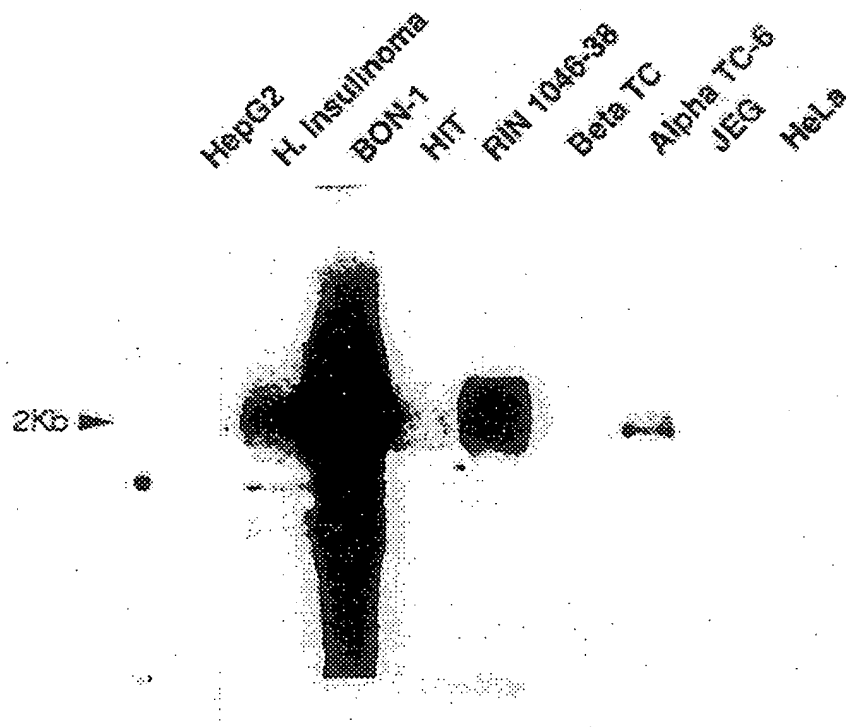


FIG. 7

